SEQUENCE LISTING

<110> Pecker, Iris

   Vlodavsky , Israel

   Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 27674

<160> 47

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

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gtagtgatgc catgtaactg aatc   24

<210> 8

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<213> Artificial sequence

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<223> Peptide derived from tryptic digestion of human heparenase

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<210> 9

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<212> DNA

<213> Homo sapiens

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cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg   180

acctggactt cttcacccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca   240

ccattgacgc caacctggcc acggacccgc ggttcctcat cctcctgggt tctccaaagc   300

ttcgtacctt ggccagaggc ttgtctcctg cgtacctgag gtttggtggc accaagacag   360

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ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt   480

tacggttgga atggccctac caggagcaat gctactccg agaacactac cagaaaaagt   540

tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct   600

caggactgga cttgatcttt ggcctaaatg cgttattaag aacagcagat ttgcagtgga   660

acagttctaa tgctcagttg ctcctggact actgctcttc caaggggtat aacatttctt   720

gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt   780

cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa   840

atgcaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga   900

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cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg   1200

tgatgaggca gtattctttt ggagcaggaa actaccattt agtggatgaa aacttcgatc   1260

ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa   1320

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tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca    1380

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tcaccaagta cttgcggtta ccctatcctt tttctaacaa gcaagtggat aaataccttc    1500

taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaactc    1560

taaagatggt ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa    1620

gttcactggg cttgccagct ttctcatata gtttttttgt gataagaaat gccaaagttg    1680

ctgcttgcat ctgaaaataa aatatactag tcctgacact g                        1721
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<210> 10

<211> 543

<212> PRT

<213> Homo sapiens

<400> 10

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            20              25              30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
            35              40              45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
        50              55              60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65              70              75              80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
            85              90              95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
            100             105             110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
        115             120             125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
        130             135             140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145             150             155             160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
                165             170             175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
            180             185             190
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Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
        195             200             205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
        210             215             220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225             230             235             240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
            245             250             255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
        260             265             270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
        275             280             285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
    290             295             300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305             310             315             320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
            325             330             335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
        340             345             350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
        355             360             365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
    370             375             380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385             390             395             400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
            405             410             415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
        420             425             430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
        435             440             445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
    450             455             460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465             470             475             480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
            485             490             495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
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               500                  505                  510

    Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
            515                 520                 525


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        530                 535                 540
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<210> 11

<211> 1721

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63)..(1691)

<223>

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   Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
   1               5                   10                  15

ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga       155
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
                20                  25                  30

cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag       203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
            35                  40                  45

ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc       251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
        50                  55                  60

aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag       299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
    65                  70                  75

ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt       347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
80                  85                  90                  95

ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc       395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
                100                 105                 110

ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc       443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
            115                 120                 125

aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa       491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
        130                 135                 140

tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag       539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
    145                 150                 155

ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act       587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
160                 165                 170                 175

ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta       635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
                180                 185                 190

tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc       683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
            195                 200                 205

ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc       731
Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
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                  210                    215                    220

aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg      779
Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
        225                    230                    235

tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag      827
Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
240                    245                    250                    255

tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct      875
Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro
                260                    265                    270

cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga      923
Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly
                275                    280                    285

gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg      971
Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg
                290                    295                    300

act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt     1019
Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
        305                    310                    315

att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct     1067
Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro
320                    325                    330                    335

ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga     1115
Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
                340                    345                    350

gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat     1163
Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
                355                    360                    365

aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa     1211
Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
                370                    375                    380

gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat     1259
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp
        385                    390                    395

cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc     1307
Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
400                    405                    410                    415

acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt     1355
Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
                420                    425                    430

cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa     1403
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
                435                    440                    445

gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac     1451
Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
                450                    455                    460

ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt     1499
Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
        465                    470                    475

cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc     1547
Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
480                    485                    490                    495

aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta     1595
Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
                500                    505                    510

atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc     1643
Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
                515                    520                    525
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tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc      1691
Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
        530                 535                 540

tgaaaataaa atatactagt cctgacactg                                     1721
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<211> 824

<212> DNA

<213> Mus musculus

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tccactgcac taacgtctat cacccacgat atcaggaagg agatctaact ctgtatgtcc      360

tgaacctcca taatgtcacc aagcacttga aggtaccgcc tccgttgttc aggaaaccag      420

tggatacgta ccttctgaag ccttcggggc cggatggatt actttccaaa tctgtccaac      480

tgaacggtca aattctgaag atggtggatg agcagaccct gccagctttg acagaaaaac      540

ctctccccgc aggaagtgca ctaagcctgc ctgcctttc ctatggtttt tttgtcataa       600

gaaatgccaa aatcgctgct tgtatatgaa aataaaaggc atacggtacc cctgagacaa      660

aagccgaggg gggtgttatt cataaaacaa aaccctagtt taggaggcca cctccttgcc      720

gagttccaga gcttcgggag ggtggggtac acttcagtat tacattcagt gtggtgttct      780

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<212> DNA

<213> Homo sapiens

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aggcgtaacg gggcggagga aaggagaaaa gggcgctggg gctcggcggg aggaagtgct      180

agagctctcg actctccgct gcgcggcagc tggcgggggg agcagccagg tgagcccaag      240

atgctgctgc gctcgaagcc tgcgctgccg ccgccgctga tgctgctgct cctggggccg      300

ctgggtcccc tctccctgg cgccctgccc cgacctgcgc aagcacagga cgtcgtggac      360

ctggacttct tcacccagga gccgctgcac ctggtgagcc cctcgttcct gtccgtcacc      420

attgacgcca acctggccac ggacccgcgg ttcctcatcc tcctgggttc tccaaagctt      480

cgtaccttgg ccagaggctt gtctcctgcg tacctgaggt ttggtggcac caagacagac      540
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caagtcaacc aggatatttg caaatatgga tccatccctc ctgatgtgga ggagaagtta   660

cggttggaat ggccctacca ggagcaattg ctactccgag aacactacca gaaaaagttc   720

aagaacagca cctactcaag aagctctgta gatgtgctat acacttttgc aaactgctca   780

ggactggact tgatctttgg cctaaatgcg ttattaagaa cagcagattt gcagtggaac   840

agttctaatg ctcagttgct cctggactac tgctcttcca aggggtataa catttcttgg   900

gaactaggca atgaacctaa cagtttcctt aagaaggctg atattttcat caatgggtcg   960

cagttaggag aagattatat tcaattgcat aaacttctaa gaaagtccac cttcaaaaat  1020

gcaaaactct atggtcctga tgttggtcag cctcgaagaa agacggctaa gatgctgaag  1080

agcttcctga aggctggtgg agaagtgatt gattcagtta catggcatca ctactatttg  1140

aatggacgga ctgctaccag ggaagatttt ctaaaccctg atgtattgga catttttatt  1200

tcatctgtgc aaaaagtttt ccaggtggtt gagagcacca ggcctggcaa gaaggtctgg  1260

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gctggcttta tgtggctgga taaattgggc ctgtcagccc gaatgggaat agaagtggtg  1380

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gcaagcgtgc aaggttcaaa gagaaggaag cttcgagtat accttcattg cacaaacact  1560

gacaatccaa ggtataaaga aggagattta actctgtatg ccataaacct ccataacgtc  1620

accaagtact tgcggttacc ctatcctttt tctaacaagc aagtggataa ataccttcta  1680

agacctttgg gacctcatgg attactttcc aaatctgtcc aactcaatgg tctaactcta  1740

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tcactgggct tgccagcttt ctcatatagt ttttttgtga taagaaatgc caaagttgct  1860

gcttgcatct gaaaataaaa tatactagtc ctgacactg                        1899
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<210> 14

<211> 592

<212> PRT

<213> Homo sapiens

<400> 14

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Arg Arg Lys Gly Arg Trp Gly Ser Ala Gly Gly Ser Ala Arg Ala Leu
            20          .           25                  30


Asp Ser Pro Leu Arg Gly Ser Trp Arg Gly Glu Gln Pro Gly Glu Pro
            35                  40                  45


Lys Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
    50                  55                  60
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Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
65   70   75   80

Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
                85   90   95

Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
            100   105   110

Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
            115   120   125

Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
    130   135   140

Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
145   150   155   160

Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
            165   170   175

Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
            180   185   190

Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
        195   200   205

Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
    210   215   220

Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
225   230   235   240

Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
            245   250   255

Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
            260   265   270

Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
        275   280   285

Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
    290   295   300

Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro
305   310   315   320

Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly
            325   330   335

Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg
            340   345   350

Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
        355   360   365

Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro

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                370                 375                 380


    Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
    385                 390                 395                 400


    Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
                        405                 410                 415


    Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
                        420                 425                 430


    Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp
                    435                 440                 445


    Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
        450                 455                 460


    Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
    465                 470                 475                 480


    Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
                    485                 490                 495


    Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
                    500                 505                 510


    Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
                515                 520                 525


    Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
        530                 535                 540


    Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
    545                 550                 555                 560


    Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
                    565                 570                 575


    Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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<210> 15

<211> 1899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94)..(1869)

<223>

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                                       Met Glu Gly Ala Val Gly Gly
                                       1                   5

gtg agg agg cgt aac ggg gcg gag gaa agg aga aaa ggg cgc tgg ggc      162
Val Arg Arg Arg Asn Gly Ala Glu Glu Arg Arg Lys Gly Arg Trp Gly
        10              15                  20

tcg gcg gga gga agt gct aga gct ctc gac tct ccg ctg cgc ggc agc      210
Ser Ala Gly Gly Ser Ala Arg Ala Leu Asp Ser Pro Leu Arg Gly Ser
    25              30              35

tgg cgg ggg gag cag cca ggt gag ccc aag atg ctg ctg cgc tcg aag      258
Trp Arg Gly Glu Gln Pro Gly Glu Pro Lys Met Leu Leu Arg Ser Lys
40              45              50                  55

cct gcg ctg ccg ccg ccg ctg atg ctg ctg ctc ctg ggg ccg ctg ggt      306
Pro Ala Leu Pro Pro Pro Leu Met Leu Leu Leu Leu Gly Pro Leu Gly
                60              65              70

ccc ctc tcc cct ggc gcc ctg ccc cga cct gcg caa gca cag gac gtc      354
Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro Ala Gln Ala Gln Asp Val
            75              80              85

gtg gac ctg gac ttc ttc acc cag gag ccg ctg cac ctg gtg agc ccc      402
Val Asp Leu Asp Phe Phe Thr Gln Glu Pro Leu His Leu Val Ser Pro
        90              95              100

tcg ttc ctg tcc gtc acc att gac gcc aac ctg gcc acg gac ccg cgg      450
Ser Phe Leu Ser Val Thr Ile Asp Ala Asn Leu Ala Thr Asp Pro Arg
    105             110             115

ttc ctc atc ctc ctg ggt tct cca aag ctt cgt acc ttg gcc aga ggc      498
Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr Leu Ala Arg Gly
120             125             130                 135

ttg tct cct gcg tac ctg agg ttt ggt ggc acc aag aca gac ttc cta      546
Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu
                140             145             150

att ttc gat ccc aag aag gaa tca acc ttt gaa gag aga agt tac tgg      594
Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe Glu Glu Arg Ser Tyr Trp
            155             160             165

caa tct caa gtc aac cag gat att tgc aaa tat gga tcc atc cct cct      642
Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser Ile Pro Pro
            170             175             180

gat gtg gag gag aag tta cgg ttg gaa tgg ccc tac cag gag caa ttg      690
Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln Glu Gln Leu
    185             190             195

cta ctc cga gaa cac tac cag aaa aag ttc aag aac agc acc tac tca      738
Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys Asn Ser Thr Tyr Ser
200             205             210             215

aga agc tct gta gat gtg cta tac act ttt gca aac tgc tca gga ctg      786
Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly Leu
                220             225             230

gac ttg atc ttt ggc cta aat gcg tta tta aga aca gca gat ttg cag      834
Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu Gln
            235             240             245

tgg aac agt tct aat gct cag ttg ctc ctg gac tac tgc tct tcc aag      882
Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys
            250             255             260

ggg tat aac att tct tgg gaa cta ggc aat gaa cct aac agt ttc ctt      930
Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Leu
    265             270             275

aag aag gct gat att ttc atc aat ggg tcg cag tta gga gaa gat tat      978
Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp Tyr
280             285             290             295
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att caa ttg cat aaa ctt cta aga aag tcc acc ttc aaa aat gca aaa       1026
Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys
                300             305             310

ctc tat ggt cct gat gtt ggt cag cct cga aga aag acg gct aag atg       1074
Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met
                315             320             325

ctg aag agc ttc ctg aag gct ggt gga gaa gtg att gat tca gtt aca       1122
Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr
                330             335             340

tgg cat cac tac tat ttg aat gga cgg act gct acc agg gaa gat ttt       1170
Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe
                345             350             355

cta aac cct gat gta ttg gac att ttt att tca tct gtg caa aaa gtt       1218
Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val
360             365             370             375

ttc cag gtg gtt gag agc acc agg cct ggc aag aag gtc tgg tta gga       1266
Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu Gly
                380             385             390

gaa aca agc tct gca tat gga ggc gga gcg ccc ttg cta tcc gac acc       1314
Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asp Thr
                395             400             405

ttt gca gct ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cga       1362
Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Arg
                410             415             420

atg gga ata gaa gtg gtg atg agg caa gta ttc ttt gga gca gga aac       1410
Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn
                425             430             435

tac cat tta gtg gat gaa aac ttc gat cct tta cct gat tat tgg cta       1458
Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp Leu
440             445             450             455

tct ctt ctg ttc aag aaa ttg gtg ggc acc aag gtg tta atg gca agc       1506
Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala Ser
                460             465             470

gtg caa ggt tca aag aga agg aag ctt cga gta tac ctt cat tgc aca       1554
Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys Thr
                475             480             485

aac act gac aat cca agg tat aaa gaa gga gat tta act ctg tat gcc       1602
Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr Ala
                490             495             500

ata aac ctc cat aac gtc acc aag tac ttg cgg tta ccc tat cct ttt       1650
Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg Leu Pro Tyr Pro Phe
505             510             515

tct aac aag caa gtg gat aaa tac ctt cta aga cct ttg gga cct cat       1698
Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro His
520             525             530             535

gga tta ctt tcc aaa tct gtc caa ctc aat ggt cta act cta aag atg       1746
Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met
                540             545             550

gtg gat gat caa acc ttg cca cct tta atg gaa aaa cct ctc cgg cca       1794
Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro
                555             560             565

gga agt tca ctg ggc ttg cca gct ttc tca tat agt ttt ttt gtg ata       1842
Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val Ile
                570             575             580

aga aat gcc aaa gtt gct gct tgc atc tgaaaataaa atatactagt             1889
Arg Asn Ala Lys Val Ala Ala Cys Ile
                585             590

cctgacactg                                                            1899
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<213> Homo sapiens

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tttttcagg caaaagtaaa atacctgaga aactgcctgg ccagaggaca atcagatttt        180

ggctggctca agtgacaagc aagtgtttat aagctagatg ggagaggaag ggatgaatac       240

tccattggag gctttactcg agggtcagag ggatacccgg cgccatcaga atgggatctg       300

ggagtcggaa acgctgggtt cccacgagag cgcgcagaac acgtgcgtca ggaagcctgg       360

tccgggatgc ccagcgctgc tccccgggcg ctcctccccg ggcgctcctc cccaggcctc       420

ccgggcgctt ggatcccggc catctccgca cccttcaagt gggtgtgggt gatttcgtaa       480

gtgaacgtga ccgccaccgg ggggaaagcg agcaaggaag taggagagag ccgggcaggc       540

ggggcggggt tggattggga gcagtgggag ggatgcagaa gaggagtggg aggg            594
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<211> 21

<212> PRT

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Ala Gly Cys Ala Thr
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<220>
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actatagggc acgcgtggt                                                  19


<210>  21
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<212>  DNA

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<220>

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<210>  33

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<212>  DNA

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<220>

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<400>  33
cgaagctctg gaactcggca ag                                                  22


<210>  34

<211>  22

<212>  DNA

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<220>

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<400>  34
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<210>  35

<211>  23

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<213>  Artificial sequence



<220>

<223>  Synthetic oligonucleotide

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aacacctgcc tcatcacgac ttc                                                 23
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<210> 36

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<220>

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<400> 36
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<210> 37

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<400> 37
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<210> 38

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<400> 38
gtaatacgac tcactatagg gc   22

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<400> 39
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<213> Homo sapiens

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ttgaactctt gggctctagt gatccacccg ccttggcctc ccaaagtgct gggattacag     180

gtgtgagcca tcacacccgg cccccgtttt ccatattagt aactcacatg tagaccacaa     240

ggatgcacta tttagaaaac ttgcaatggt ccacttttca aatcacccaa acatgttaaa     300

gaaattggta tgactgggca tggcacagtg gctcatgcct gcaatcctag cattttgtga     360

ggctgagacg ggcagatcac gaggtcagga gattgagacc atcctgacag acatggtgaa     420

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aaaaaaaaaa aaagaaagaa attggtatga ctgttgactc acaacaggag tcagggcat     660

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ctccacgtct gctaccatat tattacactc ttctggtagt gtggtgttta tgtgtgaatt     780

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ttattattat tttaagagag ggtctcactt tgtcacccag gctggagtgc agtggtgtga     960

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cagtagctgg aaccacaggc acgggccacc acgcctggct aattttttgt attttttgta    1080

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acatgctcta cagttttgcc aagtgctcgg ggttagacct gatctttggt ctaaatgcgt    1140

tactacgaac cccagactta cggtggaaca gctccaacgc ccagcttctc cttgactact    1200

gctcttccaa gggttataac atctcctggg aactgggcaa tgagcccaac agtttctgga    1260

agaaagctca cattctcatc gatgggttgc agttaggaga agactttgtg gagttgcata    1320

aacttctaca aaggtcagct ttccaaaatg caaaactcta tggtcctgac atcggtcagc    1380

ctcgagggaa gacagttaaa ctgctgagga gtttcctgaa ggctggcgga gaagtgatcg    1440

actctcttac atggcatcac tattacttga atggacgcat cgctaccaaa gaagattttc    1500

tgagctctga tgcgctggac actttttattc tctctgtgca aaaaattctg aaggtcacta    1560

aagagatcac acctggcaag aaggtctggt gggagagac gagctcagct tacggtggcg    1620

gtgcacccntt gctgtccaac acctttgcag ctggctttat gtggctggat aaattgggcc    1680

tgtcagccca gatgggcata gaagtcgtga tgaggcaggt gttcttcgga gcaggcaact    1740

accacttagt ggatgaaaac tttgagcctt tacctgatta ctggctctct cttctgttca    1800

agaaactggt aggtcccagg gtgttactgt caagagtgaa aggcccagac aggagcaaac    1860

tccgagtgta tctccactgc actaacgtct atcacccacg atatcaggaa ggagatctaa    1920

ctctgtatgt cctgaacctc cataatgtca ccaagcactt gaaggtaccg cctccgttgt    1980
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tcaggaaacc agtggatacg taccttctga agccttcggg gccggatgga ttactttcca    2040

aatctgtcca actgaacggt caaattctga agatggtgga tgagcagacc ctgccagctt    2100

tgacagaaaa acctctcccc gcaggaagtg cactaagcct gcctgccttt tcctatggtt    2160

tttttgtcat aagaaatgcc aaaatcgctg cttgtatatg aaaataaaag gcatacggta    2220

cccctgagac aaaagccgag gggggtgtta ttcataaaac aaaaccctag tttaggaggc    2280

cacctccttg ccgagttcca gagcttcggg agggtggggt acacttcagt attacattca    2340

gtgtggtgtt ctctctaaga agaatactgc aggtggtgac agttaatagc actgtg        2396
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<210> 44

<211> 535

<212> PRT

<213> Mus musculus

<400> 44

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Ala Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp
            20                  25                  30


Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe
        35                  40                  45


Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu
    50                  55                  60


Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser
65                  70                  75                  80


Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe
                85                  90                  95


Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser
            100                 105                 110


Gln Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val
        115                 120                 125


Leu Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu
    130                 135                 140


Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser
145                 150                 155                 160


Ser Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu
                165                 170                 175


Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn
                180                 185                 190


Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr
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                   195                  200                  205


Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys
    210                 215                 220


Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu
225                 230                 235                 240


Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr
                245                 250                 255


Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg
                260                 265                 270


Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His
            275                 280                 285


His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser
    290                 295                 300


Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys
305                 310                 315                 320


Val Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr
                325                 330                 335


Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala
            340                 345                 350


Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly
            355                 360                 365


Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His
    370                 375                 380


Leu Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu
385                 390                 395                 400


Leu Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys
                405                 410                 415


Gly Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val
            420                 425                 430


Tyr His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn
            435                 440                 445


Leu His Asn Val Thr Lys His Leu Lys Val Pro Pro Leu Phe Arg
    450                 455                 460


Lys Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu
465                 470                 475                 480


Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp
                485                 490                 495


Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser
                500                 505                 510
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        Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn
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        Ala Lys Ile Ala Ala Cys Ile
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        <211>  2396

        <212>  DNA

        <213>  Mus musculus


        <220>

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        <222>  (594)..(2198)

        <223>


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        ttaaggcaga agggagtcgg ggtagggtct ggctgaaccc tcaaccgggg cttttaactc       180

        agggtctagt cctggcgcca aatggatggg acctagaaaa ggtgacagag tgcgcaggac       240

        accaggaagc tggtcccacc cctgcgcggc tcccgggcgc tccctcccca ggcctccgag       300

        gatcttggat tctggccacc tccgcaccct ttggatgggt gtggatgatt tcaaaagtgg       360

        acgtgaccgc ggcggagggg aaagccagca cggaaatgaa agagagcgag gaggggaggg       420

        cggggagggg agggcgctag ggagggactc ccggggaggg tgggagggat ggagcgctgt       480

        gggagggtac tgagtcctgg cgccagaggc gaagcaggac cggttgcagg gggcttgagc       540

        cagcgcgccg gctgccccag ctctcccggc agcgggcggt ccagccaggt ggg atg        596
                                                                    Met
                                                                    1

        ctg agg ctg ctg ctg ctg tgg ctc tgg ggg ccg ctc ggt gcc ctg gcc       644
        Leu Arg Leu Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala Leu Ala
                    5                   10                  15

        cag ggc gcc ccc gcg ggg acc gcg ccg acc gac gac gtg gta gac ttg       692
        Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val Val Asp Leu
                    20                  25                  30

        gag ttt tac acc aag cgg ccg ctc cga agc gtg agt ccc tcg ttc ctg       740
        Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser Pro Ser Phe Leu
            35                  40                  45

        tcc atc acc atc gac gcc agc ctg gcc acc gac ccg cgc ttc ctc acc       788
        Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu Thr
        50                  55                  60                  65

        ttc ctg ggc tct cca agg ctc cgt gct ctg gct aga ggc tta tct cct       836
        Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser Pro
                        70                  75                  80

        gca tac ttg aga ttt ggc ggc aca aag act gac ttc ctt att ttt gat       884
        Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp
                    85                  90                  95
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ccg gac aag gaa ccg act tcc gaa gaa aga agt tac tgg aaa tct caa    932
Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser Gln
        100             105             110

gtc aac cat gat att tgc agg tct gag ccg gtc tct gct gcg gtg ttg    980
Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val Leu
    115             120             125

agg aaa ctc cag gtg gaa tgg ccc ttc cag gag ctg ttg ctg ctc cga   1028
Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg
130             135             140             145

gag cag tac caa aag gag ttc aag aac agc acc tac tca aga agc tca   1076
Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser
            150             155             160

gtg gac atg ctc tac agt ttt gcc aag tgc tcg ggg tta gac ctg atc   1124
Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile
            165             170             175

ttt ggt cta aat gcg tta cta cga acc cca gac tta cgg tgg aac agc   1172
Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser
            180             185             190

tcc aac gcc cag ctt ctc ctt gac tac tgc tct tcc aag ggt tat aac   1220
Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn
    195             200             205

atc tcc tgg gaa ctg ggc aat gag ccc aac agt ttc tgg aag aaa gct   1268
Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala
210             215             220             225

cac att ctc atc gat ggg ttg cag tta gga gaa gac ttt gtg gag ttg   1316
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu Leu
            230             235             240

cat aaa ctt cta caa agg tca gct ttc caa aat gca aaa ctc tat ggt   1364
His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr Gly
            245             250             255

cct gac atc ggt cag cct cga ggg aag aca gtt aaa ctg ctg agg agt   1412
Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg Ser
            260             265             270

ttc ctg aag gct ggc gga gaa gtg atc gac tct ctt aca tgg cat cac   1460
Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His His
    275             280             285

tat tac ttg aat gga cgc atc gct acc aaa gaa gat ttt ctg agc tct   1508
Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser Ser
290             295             300             305

gat gcg ctg gac act ttt att ctc tct gtg caa aaa att ctg aag gtc   1556
Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys Val
            310             315             320

act aaa gag atc aca cct ggc aag aag gtc tgg ttg gga gag acg agc   1604
Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser
            325             330             335

tca gct tac ggt ggc ggt gca ccc ttg ctg tcc aac acc ttt gca gct   1652
Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala Ala
            340             345             350

ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cag atg ggc ata   1700
Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly Ile
            355             360             365

gaa gtc gtg atg agg cag gtg ttc ttc gga gca ggc aac tac cac tta   1748
Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu
370             375             380             385

gtg gat gaa aac ttt gag cct tta cct gat tac tgg ctc tct ctt ctg   1796
Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu
            390             395             400

ttc aag aaa ctg gta ggt ccc agg gtg tta ctg tca aga gtg aaa ggc   1844
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            Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly
                        405             410             415

cca gac agg agc aaa ctc cga gtg tat ctc cac tgc act aac gtc tat        1892
Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr
            420             425             430

cac cca cga tat cag gaa gga gat cta act ctg tat gtc ctg aac ctc        1940
His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu
    435             440             445

cat aat gtc acc aag cac ttg aag gta ccg cct ccg ttg ttc agg aaa        1988
His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys
450             455             460             465

cca gtg gat acg tac ctt ctg aag cct tcg ggg ccg gat gga tta ctt        2036
Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu Leu
            470             475             480

tcc aaa tct gtc caa ctg aac ggt caa att ctg aag atg gtg gat gag        2084
Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp Glu
            485             490             495

cag acc ctg cca gct ttg aca gaa aaa cct ctc ccc gca gga agt gca        2132
Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser Ala
            500             505             510

cta agc ctg cct gcc ttt tcc tat ggt ttt ttt gtc ata aga aat gcc        2180
Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn Ala
    515             520             525

aaa atc gct gct tgt ata tgaaaataaa aggcatacgg tacccctgag              2228
Lys Ile Ala Ala Cys Ile
530             535

acaaaagccg aggggggtgt tattcataaa acaaaaccct agtttaggag gccacctcct     2288

tgccgagttc cagagcttcg ggagggtggg gtacacttca gtattacatt cagtgtggtg     2348

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<211> 385

<212> DNA

<213> Rattus norvegicus

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cggttcctca ccttcctgag ctctccacgg cttcgagccc tgtctagagg cttatctcct     240

gcgtacttga gatttggcgg caccaagact gacttcctta tttttgatcc caacaacgaa     300

cccacctctg aagaaagaag ttactggcaa tctcaagaca acaatgatat ttgcgggtct     360

gaccgggtct ccgctgacgt gttga                                          385
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<210> 47

<211> 541

<212> DNA

<213> Rattus norvegicus

<220>

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<222> (507)..(507)

<223> Any nucleotide

<400> 47

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cattaactgt caccacctgc agtggtctac ttagagaaca ccgcactgga tgttaacact        180

gaagcgcgtg ccccgccctc ccgaggctct ggatccagcg ttgaagcttg ccccgccctc        240

ccgaggctct ggatccagca ctggagcatg ccccgccctc ccgaggctct ggagcttgct        300

aaggagtccg ctccctaccg ctggggtttt gctttattct tatgaatgac acccctgacc        360

gctttcgtct caggggtact gtaatgcctt ttattttcat atacaagctg cgattttggc        420

atttcttatg acaaaaaacc cataggaaaa ggcgggcacg cttagtgagc ttcctgcggg        480

gagaggtttt tctgttagag ctggcanggt ctgctcatcg accatcttca ggcctcgtgc        540

c                                                                        541
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